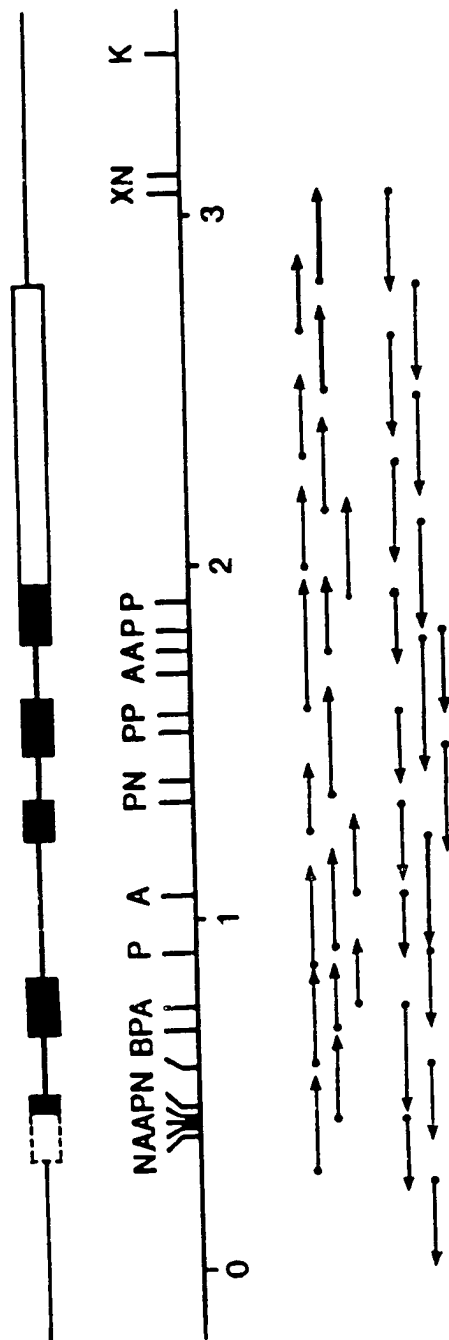


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FIG.1



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**FIG. 2A**

[illegible]

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## FIG. 2B

110 Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly  
 CTG CAG CTG GAC GTC GAC GAC TTT GCC ACC ACC ATC TGG CAG CAG ATG GAA GAA CTG GGA  
 GAC GTC GAC CTG CAG CAG CGG CTG AAA CGG TGG TGG TAG ACC GTC GTG TAC CTT CTT GAC CCT

120

130 Met Ala Pro Ala Gln Leu Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln  
 ATG GCC CCT GCC CTG CAG CCC ACC ACC CAG GGT GCC ATG CCG GCC TTC GCC TCT GCT TTC CAG  
 TAC CGG GGA CGG GAC GTC GAC GTC GGG TGG CTC CCA CGG TAC GGC CGG AAG CGA CGA AAG GTC

140

150 Arg Arg Ala Gly Gln Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr  
 CGC CGG GCA GGA GGG GTC GTC CTG GGT GCC TCC CAT CTG CAG AGC TTC CTG GAG GTG TCG TAC  
 GCG GCC CGT CCT CCC CAG GAC CAA CGG AGG GTA GAC GTC TCG AAG GAC CTC CAC AGC ATG

160

170 Arg Val Leu Arg His Leu Ala Gln Pro OP  
 CGC GTT CTA CGC CAC CTT GCC CAG CCC TGA GCC AAG CCC TCC CCA TCC CAT GTA TTT ATC  
 CGC CAA GAT GCG GTG GAA CGG GTC GGG ACT

174

TCT ATT TAA TAT TTA TGT CTA TTT AAG CCT CAT ATT TAA AGA CAG GGA AGA GCA GAA CGG

AGC CCC AGG CCT CTG TGT CCT TCC CTG CAT TTC TGA GTT TCA TTC TCC TGC CTG TAG CAG

Stul

TGA GAA AAA GCT CCT GTC CTC CCA TCC CCT GGA CTG GGA GGT AGA TAG GTA AAT ACC AAG

TAT TTA TTA CTA TGA CTG CTC CCC AGC CCT GGC TCT GCA ATG GGC ACT GGG ATG AGC CGC

TGT GAG CCC CTG GTC CTG AGG GTC CCC ACC TGG GAC CCT TGA GAG TAT CAG GTC TCC CAC

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## FIG. 2C

GTG GGA GAC AAG AAA TCC CTG TTT AAT ATT TAA ACA GCA GTG TTC CCC ATC TGG GTC CTT  
GCA CCC CTC ACT CTG GCC TCA GCC GAC TGC ACA GCG GCC CCT GCA TCC CCT TGG CTG TGA  
GGC CCC TGG ACA AGC AGA GGT GGC CAG AGC TGG GAG GCA TGG CCC TGG GGT CCC ACG AAT  
TTG CTG GGG AAT CTC GTT TTT CTT AAG ACT TTT GGG ACA TGG TTT GAC TCC CGA ACA  
TCA CCG ACG TGT CTC CTG TTT TTC TGG GTG GCC TCG GGA CAC CTG CCC TGC CCC CAC GAG  
GGT CAG GAC TGT GAC TCT TTT TAG GGC CAG GCA GGT GCC TGG ACA TTT GCC TTG CTG GAC  
GGG GAC TGG GGA TGT GGG AGG GAG CAG ACA GGA GGA ATC ATG TCA GGC CTG TGT GTG AAA  
GGA AGC TCC ACT GTC ACC CTC CAC CTC TTC ACC CCC CAC TCA CCA GTG TCC CCT CCA CTG  
TCA CAT TGT AAC TGA ACT TCA GGA TAA TAA AGT GTT TGC CTC CA

[f150-200 base poly A plus 25-30 bases plasmid DNA preceding a PvuII restriction site]-3'

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GGGGACAGGCTTGAGAAATCCCAAAGGAGAGGGGCAAGGACACTGCCCCCGCAAGTCTGCCAGAGCAGAG 70  
AGGGAGACCCCGACTCAGCTGCCACTTCCCCACAGGCTCGTGCCGCTTCCAGGCGTCTATCAGCGGCTCA 140  
GCCTTGTTCAGCTGTTCTGTCAAACA CTCTGGGGCCATT CAGGCCCTGGGTGGGCAGCGGGAGGAAGG 210  
GAGTTGAGGGGGGCAAGCGACGTCAAAGGAGGATCAGAGATTCACAAATTTACAAAACTTTCGCAAA 280  
CAGCTTTTGTTCCAAACCCCTTGCAATTGCTTGGACACCAAATTTGCATAAAATCCTGGGAAGTTATTAC 350  
TAAGCCTTAGTCGTGGCCCCCAGGTAATTTCTCCAGGCCCTCCATGGGGTTATGTATAAAGGCCCCCTTA 420  
GAGCTGGGCCCCAAAACAGCCCCGGAGCCTGCAGCCCCCAGCCCCACCCAGACCCCATGGCTGGACCTGCCACC 490  
GlnSerProMetLysLeuMeta  
CAGAGCCCATGAAGCTGATGGGTGAGTGTCTTGGCCCCAGGATGGGAGAGCCGCTGCCCTGGCATGGGA 560  
GGGAGGCTGGTGTACAGAGGGGCTGGGGATCCCCGTTCTGGGAATGGGGATTAAAGGCACCCAGTGTCC 630  
CCGAGAGGGCCTCAGGTGGTAGGGAACAGCATGTCTCCTGAGCCCCGCTCTGTCCCCCAGCCCTGCAGCTGC 700  
laLeuGlnLeuL

FIG. 3A

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-10	-1	+	10
euLeuTrpHisSerAlaLeuTrpThrValGlnGluAlaThrProLeuGlyProAlaSerSerLeuProGlu			770
TGCTGTGGCACAGTGCACTCTGGACAGTGCAGGAAGCACCCCTGGGCCCTGCCAGCTCCTGTGCCCA			
	20	30	
nSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLys			840
GAGCTTCCTGCTCAAGTGCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAG			
35			910
Leu			
CTGGTGAGTGAGGTGGGTGAGAGGGCTGTGGAGGGAAGCCCGTGGGGAGAGCTAAGGGGGATGGAACTG			
CAGGGCCAACATCCTCTGGAAAGGACATGGGAGAATATTAGGAGCATGGAGCTGGGGAAGGCTGGGAAG			980
GGACTTGGGGAGGAGGACCTTGGTGGGGACAGTGCTCGGGAGGGCTGGCTGGGATGGGAGTGGAGGCATC			1050
ACATTCAGGAGAAAGGCAAGGGCCCTGTGTGAGATCAGAGAGTGGGGTGCGAGGCAGAGAGGAACTGAA			1120
CAGCCTGGCAGGACATGGAGGGAGGGGAAAGACCAGAGAGTCGGGGAGGACCCGGGAAGGAGCGGCGACC			1190
	36	40	
CysAlaThrTyrLysLeuCysHisProGlu			
CGGCCACGGCGAGTCTCACTCAGCATCCTTCCATCCCCAGTGTGCCACCTACAAGCTGTGCCACCCCGAG			1260
	60		
GluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaIle			1330
GAGCTGGTGCTCGGACACTCTCTGGGCATCCCCCTGGGCTCCCCAGTGTGCCACCCAGCGCCC			

**FIG. 3B**

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70 71  
euGlnLeu 1400  
TGCAGCTGGTGAGTGCAGGAAAGGATAAGGCTAATGAGGAGGGGGAAGGAGAGGAAACACCCATGGG  
1470  
CTCCCCCATGTCTCCAGGTTCCAAGCTGGGGGCTGACGTATCTCAGGCAGCACCCCTAACTCTTCCGC  
90  
72  
AlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnA  
80  
TCTGTCTCACAGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCCTTTCTCTACCAAGGGCTCCTGCAGG  
1540  
110  
laLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAl  
100  
CCCTGGAAAGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTGCGCGACTTTGC  
1610  
120  
aThrThrIleTrpGlnGln  
CACCACCATCTGGCAGCAGGTGAGCCCTTGTGGCAGGGTGGCCCAAGTCTGCTGGCATTTCTGGGCACC  
1680  
121  
ACAGCCGGCCCTGTGTATGGGCCCTGTCCATGCTGTGTCAGCCCCCAGCATTTCCCTCATTTGTATAACGCC  
1750  
150  
CACTCAGAAAGGGCCCAACCACTGATCACAGCTTTCCCCCACCAGATGGAAGAACTGGGAATGGCCCCCTGCC  
MetGluGluLeuGlyMetAlaProAla  
140  
130  
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgAlaGlyGlyValLeuV  
1890  
CTGCAGCCCCACCCAGGGTGCCATGCCGGCCTTCGCCCTCTGCTTCCAGCGCCGGCAGGAGGGTCCCTGG

FIG. 3C

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160 170 174  
alAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProOP 1960  
TTGCCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCCAGCCCTGAGC  
2030  
CAAGCCCTCCCCATCCCATGTATTTATCTCTATTTAATAATTTATGTCTATTTAAGCCTCATATTTAAAGA  
2100  
CAGGGAAGAGCAGAACGGAGCCCCAGGCCCTCTGTGTCTTCCCCTGCATTTCTGAGTTTCATTTCTCCTGCC  
2170  
TGTAGCAGTGAGAAAAAGCTCCTGTCTCTCCATCCCTGGACTGGGAGGTAGATAGGTAATAACCAAGTA  
2240  
TTTATTACTATGACTGCTCCCCAGCCCCCTGGCTCTGCAATGGGCACTGGGATGAGCCGCTGTGAGCCCCCTG  
2310  
GTCCTGAGGGTCCCCACCTGGGACCCCTTGAGAGTATCAGGTCTCCACGCTGGGAGACAAGAAATCCCTGT  
2380  
TTAATAATTTAAACAGCAGTGTTCCTCCCATCTGGGTCTTGCACCCCCTCACTCTGGCCTCAGCCGACTGCAC  
2450  
AGCGGCCCTGCATCCCCCTTGGCTGTGAGGCCCTGGACAAGCAGAGGTGGCCAGAGCTGGGAGGCATGG  
2520  
CCCTGGGGTCCCACGAATTGCTGGGGAATCTCGTTTCTTCTTAAAGACTTTTGGGACATGGTTTGACT  
2590  
CCCGAACATCACCGACGTGTCTCCTGTTTTTCTGGGTGGCCTCGGGACACCTGCGCCTGCCCCACGAGGG

FIG. 3D



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TCAGGACTGTGACTCTTTTAGGGCCAGGCAGGTGCCCTGGACATTTGCCCTTGCTGGATGGGGACTGGGGA 2660

TGTGGGAGGGAGCAGACAGGAGGAATCATGTCAGGCCCTGTGTGTGAAAGGAAGCTCCACTGTCAACCTCC 2730

ACCTCTTCACCCCCACTCAACAGTGTCCCCCTCCACTGTCAATGTAACTGAACCTTCAGGATAATAAAG 2800

TGTTTGCCCTCCAGTCACGTCCTTCCCTCCTTCTTGAGTCCAGCTGGTGCCCTGGCCAGGGGCTGGGGAGGTG 2870

GCTGAAGGGTGGGAGAGGCCAGAGGGAGGTCGGGGAGGAGGTCCTGGGAGGAGGTCCAGGGAGGAGGAGG 2940

AAAGTTCTCAAGTTCGTCTGACATTCAATTCGTTAGCACATATTTATCTGAGCACCTACTCTGTGCAGAC 3010

GCTGGGCTAAGTGCTGGGGACACAGCAGGGGAACAAGGCAGACATGGAATCTGCACTCGAG 3070

FIG. 3E

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## FIG. 4

## EChpG-CSFDNA SECTION I

10      1      20      30      40      50      60  
 CTAGAAAA ACCAAGGAGG TAATAAATAA TGACTCCATT AGGTCCTGGT TCTTCTCTGC  
 TTTT TGGTTCCTCC ATTATTTATT ACTGAGGTAA TCCAGGACGA AGAAGAGACG

8

XbaI

70      3      80      90      100      110      120  
 CGCAAGCCTT TCTGCTGAAA TGTCCTGGAAC AGGTTCTGTAA AATCCAGGGT GACGGTGCTG  
 GCGTTTCGAA AGACGACTTT ACAGACCTTG TCCAAGCATT TTAGGTCCCA CTGCCACGAC

10

11

130      5      140      150      160      170      180  
 CACTGCAAGA AAAACTGTGC GCTACTTACA AACTGTGCCA TCCGGAAGAG CTGGTACTGC  
 GTGACGTTCT TTTTGACACG CGATGAATGT TTGACACGGT AGGCCTTCTG GACCATGACG

12

13

7      190      100  
 TGGTCATTC TCTTGG  
 ACCCAGTAAG AGAACCCCTAG

14

BamHI

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## FIG. 5

## EChpG-CSFDNA SECTION II

10 15 20 30 40 50 60  
 GATCCCGTG GGCTCCGCTG TCTTCTTGTC CATCTCAAGC TCTTCAGCTG GCTGGTTGTC  
 GGCAC CCGAGGCGAC AGAAGAACAG GTAGAGTTCTG AGAAGTCGAC CGACCAACAG  
 23 24

BamHI

70 17 80 90 110 120  
 TGCTCTCAACT GCATTCCTGGT CTGTTCCCTGT ATCAGGGTCT TCTGCAAGCT CTGGAAGGTA  
 ACAGAGTTGA CGTAAGACCA GACAAGGACA TAGTCCCAGA AGACGTTCTGA GACCTTCCAT  
 25 26 27

130 140 150 160 170 180  
 TCTCTCCGGA ACTGGGTCCG ACTCTGGACA CTCTGCAGCT AGATGTAGCT GACTTTGCTA  
 AGAGAGGCCT TGACCCAGGC TGAGACCTGT GAGACGTCTGA TCTACATCGA CTGAACCGAT  
 28 29

190 200 210  
 CTAATAATTG GCAACAGATG GAAGAGCTCA AAG  
 GATGATAAAC CGTGTCTAC CTCTCTCGAGT TTCTTTAA  
 30 SstI EcoRI

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## FIG. 6

## EChpG-CSFDNA SECTION III

10 31 20 30 40 50 60  
 GATCCAAAG AGCTCGGTAT GGCACCAGCT CTGCAACCGA CTCAAAGGTGC TATGCCGGCA  
 GTTTC TCGAGCCATA CCGTGGTCGA GACGTTGGCT GAGTTCACG ATACGGCCGT

38BamHI SstI

70 33 80 90 100 110 120  
 TTCGCTTCTG CATTCAGCG TCGTGCAGGA GGTGACTGG TTGCTTCTCA TCTGCAATCT  
 AAGCGAAGAC GTAAGGTCGC AGCAGTCCT CCACATGACC AACGAAGAGT AGACGTTAGA

4039

35 130 140 150 160 170  
 TTCCTGGAAG TATCTTACCG TGTTCTGCGT CATCTGGCTC AGCCGTAATA G  
 AAGGACCTTC ATAGAATGGC ACNAGACGCA GTAGACCGAG TCGGCATTAT CTAA

4241EcoRI

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**FIG. 7A**

[illegible]

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FIG. 7B

[illegible]

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## FIG. 8

1 ATCGATTGATTCTAGAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCCGGTACCAT  
TAGCTAAACTAAGATCTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCCATGGTA  
1 Clal, 12 XbaI, 29 NdeI, 35 HincII, HpaI, 39 MluI, 47 EcoRI,  
53 HgiCI KpnI, 57 NcoI SlyI,  
61 GGAAGCTTACTCGAGGATCCGCGGATAAATAAGTAACGATCC  
CCTTCGAATGAGCTCCTAGGCGCCTATTATTTCATTTGCTAGG  
63 HindIII, 70 AvaI XhoI, 75 BamHI Xho2, 79 Sac2,

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Competitor	(U/ml)	WEHI-3B (D <sup>+</sup> )		ANLL (M4)		ANLL (M5B)	
		cpm	% Inhib.	cpm	% Inhib.	cpm	% Inhib.
<u>Exp. 1</u>							
none	0	6,608	-	1,218	-	122	-
natural							
hpG-CSF:							
	10,000	685	90				
	2,000	1,692	74	34	97	-376	0
	200	2,031	69				
	10,000	0	100				
	2,000	1,185	82	202	83	0	0
	200	2,330	65				
rhpG-CSF:							
<u>Exp. 2</u>							
none	0	2,910	0				
natural							
hpG-CSF:	2,000	628	78				
GM-CSF:	2,000	3,311	0				

FIG. 9